What Is Claimed Is:

1. A method of identifying the haplotype of an organism, the method comprising:

(a) providing a sample comprising nucleic acids from the organism, wherein the nucleic acids comprise at least two copies of an isogenic nucleotide sequence of interest,

(b) aliquotting the nucleic acids into test locations such that at least one test location is expected to contain one, and only one, isogenic nucleotide sequence of interest,

(c) amplifying the isogenic nucleotide sequence of interest in a predetermined number of test locations to create amplification products,

(i) wherein amplifying the isogenic nucleotide sequence of interest employs two pairs of oligonucleotide primers

(ii) such that at least one test location is expected to contain amplification products having a unique nucleotide sequence corresponding to the nucleotide sequence of one, and only one, of the isogenic nucleotide sequences of interest in the organism's genome, and

(d) detecting the presence or absence of specific forms of a first nucleotide polymorphism and a second nucleotide polymorphism in the isogenic region of interest at two non-contiguous positions in the nucleotide sequence of interest by detecting the presence or absence of specific forms of the first nucleotide polymorphism and second nucleotide polymorphism in the amplification products in each of the predetermined number of test locations comprising amplified nucleic acids,

such that the haplotype of the organism is identified.

2. The method of claim 1, wherein on average less than about 1 copy of the isogenic region of interest is aliquotted into each test location.

3. The method of claim 2, wherein on average less than about 0.67 copies of the isogenic region of interest is aliquotted into each test location.

4. The method of claim 2, wherein on average from about 0.4 copies to about 0.6 copies of the isogenic region of interest is aliquotted into each test location.

5. The method of claim 1, wherein the step of amplifying the isogenic region of interest employs a duplexed or multiplexed method selected from the group consisting of Qβ replicase mediated amplification, ligase chain reaction, NASBA, and transcription mediated amplification.

6. The method of claim 1, wherein the step of amplifying the isogenic region of interest employs multiplexed polymerase chain reaction.

7. The method of claim 1, wherein

at least about 1 kilobase of nucleotide sequence in the isogenic region of interest separates the nucleotide sequences in the isogenic region of interest that are complementarity to an oligonucleotide primer of (i) the first oligonucleotide primer pair and (ii) an oligonucleotide primer of the second primer pair.

8. The method of claim 7, wherein

at least about 5 kilobases of nucleotide sequence in the isogenic region of interest separates the nucleotide sequences in the isogenic region of interest that are complementarity to an oligonucleotide primer of (i) the first oligonucleotide primer pair and (ii) an oligonucleotide primer of the second primer pair.

9. The method of claim 1, wherein the step of detecting the absence or presence of a particular polymorphism employs a probe.

10. The method of claim 9, wherein said probe is a molecular beacon probe.

11. The method of claim 1, wherein the sample comprising nucleic acids from the organism comprises genomic DNA.

12. The method of claim 1, wherein the sample comprising nucleic acids from the organism comprises cDNA.

13. The method of claim 1, wherein the sample comprising nucleic acids from the organism comprises isogenic polymerase chain reaction products.

14. The method of claim 1, wherein a test location is a well of a multi-well test plate.

15. The method of claim 1, wherein a test location is an isolated position in an array.

16. The method of claim 15, wherein the array is formed by a reagent jetting system.

17. The method of claim 1, wherein the organism is human and the haplotype identified is a TPMT haplotype.

18. The method of claim 17, wherein the method distinguishes between the *1/*3A and *3B/*3C combinations of haplotypes.

19. A kit, useful for identifying the haplotype of an organism having a diploid genome, comprising:

(a) a first pair of oligonucleotides,

(b) a second pair of oligonucleotides,

wherein

(i) the first pair of oligonucleotides are complementary to a nucleotide sequence flanking a first polymorphism in an isogenic region of the organism's genome

(ii) the second pair of oligonucleotides are complementary to a nucleotide sequence flanking a second polymorphic site in an isogenic region of the organism's genome

(iii) no oligonucleotide of the first pair or second pair of oligonucleotides is complementary to a nucleotide sequence in the isogenic nucleotide sequence of interest that is complementary to another oligonucleotide of the first pair or second pair of oligonucleotides

(c) a first probe specific for the first polymorphism within a first isogenic nucleotide sequence of interest, and

(d) a second probe specific for the second polymorphism within a second isogenic nucleotide sequence of interest.

20. The kit of claim 19 further comprising an enzyme selected from the group consisting of DNA polymerases, RNA polymerases, ligases, and phage replicases.

21. The kit of claim 19 further comprising a third pair of oligonucleotides, wherein the third pair of oligonucleotides are complementary to a nucleotide sequence flanking a third polymorphic site in an isogenic region of the organism's genome.

22. A kit, useful for identifying the haplotype of an organism having a diploid genome, comprising:

(a) a first pair of oligonucleotides,

(b) a second pair of oligonucleotide,

wherein

(i) the first pair of oligonucleotides are complementary to a nucleotide sequence flanking a first polymorphism in an isogenic region of the organism's genome

(ii) the second pair of oligonucleotides are complementary to a nucleotide sequence flanking a second polymorphic site in an isogenic region of the organism's genome

(iii) no oligonucleotide of the first pair or second pair of oligonucleotides is complementary to a nucleotide sequence in the isogenic nucleotide sequence of

interest that is complementary to another oligonucleotide of the first pair or second pair of oligonucleotides

(c) a means of detecting one or more specific forms of a first polymorphism within a first isogenic nucleotide sequence of interest, and

(d) a means of detecting one or more specific forms of a second polymorphism within a second isogenic nucleotide sequence of interest.